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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/913,858A

DATE: 04/09/2003

TIME: 11:30:17

Input Set : A:\030560-057.ST25.txt

Output Set: N:\CRF4\04092003\I913858A.raw

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4 <110> APPLICANT: Altmann, Friedrich
6 <120> TITLE OF INVENTION: Fucosyl Transferase Gene
8 <130> FILE REFERENCE: 030560-057
10 <140> CURRENT APPLICATION NUMBER: US 09/913,858A
11 <141> CURRENT FILING DATE: 2001-08-20
13 <150> PRIOR APPLICATION NUMBER: PCT/AT00/00040
14 <151> PRIOR FILING DATE: 2000-02-17
16 <150> PRIOR APPLICATION NUMBER: AT A 270/99
17 <151> PRIOR FILING DATE: 1999-02-18
19 <160> NUMBER OF SEQ ID NOS: 17
21 <170> SOFTWARE: PatentIn version 3.1
23 <210> SEQ ID NO: 1
25 <211> LENGTH: 2198
26 <212> TYPE: DNA
27 <213> ORGANISM: Unknown Organism
29 <220> FEATURE:
30 <223> OTHER INFORMATION: Description of Unknown Organism:plant
32 <400> SEQUENCE: 1
33 actaactcaa acgctgcatt ttcttttttc ttccaggga ccatccaccc ataacaacaa 60
34 aaaaaacaac agcaagctgt gtttttttta tcgttctttt tctttaaaca agcaccacca 120
35 tcatggaatc gtgctcataa cgccaaaatt ttccatttcc ctttgatttt tagtttattt 180
36 tgcggaattg gcagttgggg ggcgaattga atgatgggtc tgttgacgaa tcttcgaggc 240
37 tcgagaacag atggtgccca acaagacagc ttaccggttt tggctccggg aggcaaccca 300
38 aagaggaaat ggagcaatct aatgcctctt gttgttgccc ttgtggtcat cgcgagatc 360
39 gcgtttctgg gtaggttgga tatggccaaa aacgcgcgca tgggtgactc cctcgtgac 420
40 ttctttctacc gctctcgagc ggtcgttgaa ggtgacgatt tggggttggg tttggtggct 480
41 tctgatcgga attctgaatc gtatagttgt gaggaatggt tggagaggga ggatgctgtc 540
42 acgtattcga ggggcttttc caaagagcct atttttgttt ctggagctga tcaggagtgg 600
43 aagtcgtggt cggttggtg taaatttggg tttagtgggg atagaaagcc agatgccgca 660
44 tttgggttac ctcaaccaag tggaacagct agcattctgc gatcaatgga atcagcagaa 720
45 tactatgctg agaacaatat tgccatggca agacggaggg gatataacat cgtaatgaca 780
46 accagtctat cttcggatgt tcctgttgga tatttttcat gggctgagta tgatatgatg 840
47 gcaccagtgc agccgaaaac tgaagctgct cttgcagctg ctttcatttc caattgtggt 900
48 gctcgaaatt tccggttgca agctcttgag gcccttgaaa aatcaaacat caaaattgat 960
49 tcttatggtg gttgtcacag gaaccgtgat ggaagagtga acaaagtgga agccctgaag 1020
50 cactacaaat tttagcttagc gtttgaaaat tcgaatgagg aagattatgt aactgaaaaa 1080
51 ttcttccaat cccttggtgc tggaactgtc cctgtggttg ttggtgctcc aaatatcag 1140
52 gactttgctc cttctcctgg ttcaatttta catattaaag agatagagga tgttgagtct 1200
53 gttgcaaaga ccatgagata tctagcagaa aatcccgaag catataatca atcattgagg 1260
54 tggaagtatg agggctccatc tgactccttc aaggcccttg tggatatggc agctgtgcat 1320
55 tcatcgtgcc gtctttgcat tcacttgcc acagtgahta gagagaagga agaaaataat 1380
56 ccaagcctta agagacgtcc ttgcaagtgc actagagggc cagaaaccgt atatcatatc 1440
57 tatgtcagag aaaggggaag gtttgagatg gagtccattt acctgagggtc tagcaattta 1500

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58 actctgaatg ctgtgaaggc tgctgttggt ttgaagttca catccctgaa tcttgtgcct 1560
59 gtatggaaga ctgaaaggcc tgaagttata agagggggga gtgctttaaa actctacaaa 1620
60 atatacccaa ttggcttgac acagagacaa gctctttata ccttcagctt caaagggtgat 1680
61 gctgatttca ggagtcactt ggagaacaat ccttgtgcca agtttgaagt catttttgtg 1740
62 tagcatgcgc taaatggtag ctctgtctta cctgaattag cttcacttag ctgagcacta 1800
63 gctagagttt taggaatgag tatggcagtg aatatggcat ggctttattt atgcctagtt 1860
64 tcttggccaa ctcatgatg ttttgtataa gacatcacac ttttaatttta aacttgtttc 1920
65 tgtagaagtg caaatccata tttaatgctt agtttttagtg ctcttatctg atcatctaga 1980
66 agtcacagtt cttgtatatt gtgagtgaata actgaaatct aatagaagga tcagatgttt 2040
67 cactcaagac acattattac ttcattgtgt tttgatgatc tcgagctttt ttagtgtctg 2100
68 gaactgtccc tgtggtttga gcacctgtta ttgcttcagt gttactgtcc agtggttatc 2160
69 gtttttgacc tctaaaaaaaa aaaaaaaaaa aaaaaaaaaa - - - 2198

```

71 &lt;210&gt; SEQ ID NO: 2

72 &lt;211&gt; LENGTH: 510

73 &lt;212&gt; TYPE: PRT

74 &lt;213&gt; ORGANISM: Unknown Organism

76 &lt;220&gt; FEATURE:

77 &lt;223&gt; OTHER INFORMATION: Description of Unknown Organism:plant

79 &lt;400&gt; SEQUENCE: 2

```

80 Met Met Gly Leu Leu Thr Asn Leu Arg Gly Ser Arg Thr Asp Gly Ala
81 1 5 10 15
83 Gln Gln Asp Ser Leu Pro Val Leu Ala Pro Gly Gly Asn Pro Lys Arg
84 20 25 30
86 Lys Trp Ser Asn Leu Met Pro Leu Val Val Ala Leu Val Val Ile Ala
87 35 40 45
89 Glu Ile Ala Phe Leu Gly Arg Leu Asp Met Ala Lys Asn Ala Ala Met
90 50 55 60
92 Val Asp Ser Leu Ala Asp Phe Phe Tyr Arg Ser Arg Ala Val Val Glu
93 65 70 75 80
95 Gly Asp Asp Leu Gly Leu Gly Leu Val Ala Ser Asp Arg Asn Ser Glu
96 85 90 95
98 Ser Tyr Ser Cys Glu Glu Trp Leu Glu Arg Glu Asp Ala Val Thr Tyr
99 100 105 110
101 Ser Arg Gly Phe Ser Lys Glu Pro Ile Phe Val Ser Gly Ala Asp Gln
102 115 120 125
104 Glu Trp Lys Ser Cys Ser Val Gly Cys Lys Phe Gly Phe Ser Gly Asp
105 130 135 140
107 Arg Lys Pro Asp Ala Ala Phe Gly Leu Pro Gln Pro Ser Gly Thr Ala
108 145 150 155 160
110 Ser Ile Leu Arg Ser Met Glu Ser Ala Glu Tyr Tyr Ala Glu Asn Asn
111 165 170 175
113 Ile Ala Met Ala Arg Arg Arg Gly Tyr Asn Ile Val Met Thr Thr Ser
114 180 185 190
116 Leu Ser Ser Asp Val Pro Val Gly Tyr Phe Ser Trp Ala Glu Tyr Asp
117 195 200 205
119 Met Met Ala Pro Val Gln Pro Lys Thr Glu Ala Ala Leu Ala Ala Ala
120 210 215 220
122 Phe Ile Ser Asn Cys Gly Ala Arg Asn Phe Arg Leu Gln Ala Leu Glu
123 225 230 235 240

```

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```

125 Ala Leu Glu Lys Ser Asn Ile Lys Ile Asp Ser Tyr Gly Gly Cys His
126                245                250                255
128 Arg Asn Arg Asp Gly Arg Val Asn Lys Val Glu Ala Leu Lys His Tyr
129                260                265                270
131 Lys Phe Ser Leu Ala Phe Glu Asn Ser Asn Glu Glu Asp Tyr Val Thr
132                275                280                285
134 Glu Lys Phe Phe Gln Ser Leu Val Ala Gly Thr Val Pro Val Val Val
135                290                295                300
137 Gly Ala Pro Asn Ile Gln Asp Phe Ala Pro Ser Pro Gly Ser Ile Leu
138 305                310                315                320
140 His Ile Lys Glu Ile Glu Asp Val Glu Ser Val Ala Lys Thr Met Arg
141                325                330                335
143 Tyr Leu Ala Glu Asn Pro Glu Ala Tyr Asn Gln Ser Leu Arg Trp Lys
144                340                345                350
146 Tyr Glu Gly Pro Ser Asp Ser Phe Lys Ala Leu Val Asp Met Ala Ala
147                355                360                365
149 Val His Ser Ser Cys Arg Leu Cys Ile His Leu Ala Thr Val Ser Arg
150                370                375                380
152 Glu Lys Glu Glu Asn Asn Pro Ser Leu Lys Arg Arg Pro Cys Lys Cys
153 385                390                395                400
155 Thr Arg Gly Pro Glu Thr Val Tyr His Ile Tyr Val Arg Glu Arg Gly
156                405                410                415
158 Arg Phe Glu Met Glu Ser Ile Tyr Leu Arg Ser Ser Asn Leu Thr Leu
159                420                425                430
161 Asn Ala Val Lys Ala Ala Val Val Leu Lys Phe Thr Ser Leu Asn Leu
162                435                440                445
164 Val Pro Val Trp Lys Thr Glu Arg Pro Glu Val Ile Arg Gly Gly Ser
165                450                455                460
167 Ala Leu Lys Leu Tyr Lys Ile Tyr Pro Ile Gly Leu Thr Gln Arg Gln
168 465                470                475                480
170 Ala Leu Tyr Thr Phe Ser Phe Lys Gly Asp Ala Asp Phe Arg Ser His
171                485                490                495
173 Leu Glu Asn Asn Pro Cys Ala Lys Phe Glu Val Ile Phe Val
174                500                505                510

```

177 &lt;210&gt; SEQ ID NO: 3

178 &lt;211&gt; LENGTH: 105

179 &lt;212&gt; TYPE: DNA

180 &lt;213&gt; ORGANISM: Artificial Sequence

182 &lt;220&gt; FEATURE:

183 &lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: GlcNAc-alpha1,3-fucosyl

185 &lt;400&gt; SEQUENCE: 3

186 gaagccctga agcactacaà atttagctta gcgtttgaaa attcgaatga ggaagattat 60

187 gtaactgaaa aattcttcca atcccttggt gctggaactg tccct 105

189 &lt;210&gt; SEQ ID NO: 4

190 &lt;211&gt; LENGTH: 35

191 &lt;212&gt; TYPE: PRT

192 &lt;213&gt; ORGANISM: Artificial Sequence

194 &lt;220&gt; FEATURE:

195 &lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Mung bean

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```

197 <400> SEQUENCE: 4
198 Glu Ala Leu Lys His Tyr Lys Phe Ser Leu Ala Phe Glu Asn Ser Asn
199   1           5           10           15
201 Glu Glu Asp Tyr Val Thr Glu Lys Phe Phe Gln Ser Leu Val Ala Gly
202           20           25           30
204 Thr Val Pro
205           35
208 <210> SEQ ID NO: 5
209 <211> LENGTH: 15
210 <212> TYPE: PRT
211 <213> ORGANISM: Artificial Sequence
213 <220> FEATURE:
214 <223> OTHER INFORMATION: Description of Artificial Sequence:n-terminal sequence
215   of tryptic peptide
217 <220> FEATURE:
218 <221> NAME/KEY: MISC FEATURE
219 <222> LOCATION: (5)..(5)
220 <223> OTHER INFORMATION: Xaa = any amino acid
222 <400> SEQUENCE: 5
W--> 224 Lys Pro Asp Ala Xaa Phe Gly Leu Pro Gln Pro Ser Thr Ala Ser
225   1           5           10           15
230 <210> SEQ ID NO: 6
231 <211> LENGTH: 10
232 <212> TYPE: PRT
233 <213> ORGANISM: Artificial Sequence
235 <220> FEATURE:
236 <223> OTHER INFORMATION: Description of Artificial Sequence:n-terminal sequence
237   of tryptic peptide
239 <400> SEQUENCE: 6
240 Pro Glu Thr Val Tyr His Ile Tyr Val Arg
241   1           5           10
244 <210> SEQ ID NO: 7
245 <211> LENGTH: 13
246 <212> TYPE: PRT
247 <213> ORGANISM: Artificial Sequence
249 <220> FEATURE:
250 <223> OTHER INFORMATION: Description of Artificial Sequence:n-terminal sequence
251   of tryptic peptide
253 <400> SEQUENCE: 7
254 Met Glu Ser Ala Glu Tyr Tyr Ala Glu Asn Asn Ile Ala
255   1           5           10
258 <210> SEQ ID NO: 8
259 <211> LENGTH: 10
260 <212> TYPE: PRT
261 <213> ORGANISM: Artificial Sequence
263 <220> FEATURE:
264 <223> OTHER INFORMATION: Description of Artificial Sequence:n-terminal sequence
265   of tryptic peptide
267 <400> SEQUENCE: 8

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```

268 Gly Arg Phe Glu Met Glu Ser Ile Tyr Leu
269   1           5           10
271 <210> SEQ ID NO: 9
272 <211> LENGTH: 29
273 <212> TYPE: DNA
274 <213> ORGANISM: Artificial Sequence
276 <220> FEATURE:
277 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
279 <220> FEATURE:
280 <221> NAME/KEY: misc_feature
281 <222> LOCATION: (3)..(15)
282 <223> OTHER INFORMATION: n = any nucleotide
284 <400> SEQUENCE: 9
W--> 285 gcngartayt aygcngaraa yaayathgc 29
288 <210> SEQ ID NO: 10
289 <211> LENGTH: 22
290 <212> TYPE: DNA
291 <213> ORGANISM: Artificial Sequence
293 <220> FEATURE:
294 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
296 <220> FEATURE:
297 <221> NAME/KEY: misc_feature
298 <222> LOCATION: (14)..(17)
299 <223> OTHER INFORMATION: n = any nucleotide
301 <400> SEQUENCE: 10
W--> 302 crtadatrtg rtanacngty tc 22
305 <210> SEQ ID NO: 11
306 <211> LENGTH: 20
307 <212> TYPE: DNA
308 <213> ORGANISM: Artificial Sequence
310 <220> FEATURE:
311 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
313 <220> FEATURE:
314 <221> NAME/KEY: misc_feature
315 <222> LOCATION: (6)..(6)
316 <223> OTHER INFORMATION: n = any nucleotide
318 <400> SEQUENCE: 11
W--> 319 tadatnswyt ccatytcraa 20
322 <210> SEQ ID NO: 12
323 <211> LENGTH: 20
324 <212> TYPE: DNA
325 <213> ORGANISM: Artificial Sequence
327 <220> FEATURE:
328 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
330 <400> SEQUENCE: 12
331 ctggaactgt ccctgtggtt 20
333 <210> SEQ ID NO: 13
334 <211> LENGTH: 20
335 <212> TYPE: DNA

```

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/913,858A

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; Xaa Pos. 5  
Seq#:9; N Pos. 3,15  
Seq#:10; N Pos. 14,17  
Seq#:11; N Pos. 6

## VERIFICATION SUMMARY

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L:224 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0  
L:285 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0  
L:302 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0  
L:319 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0

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